SEQUENCE LISTING

(1) GENERAL INFORMATION

5   (i) APPLICANT: DEEN, KEITH C

                        YOUNG, PETER R

      (ii) TITLE OF THE INVENTION: TUMOR NECROSIS FACTOR RELATED
            RECEPTOR, TR6

10

      (iii) NUMBER OF SEQUENCES: 4

      (iv) CORRESPONDENCE ADDRESS:

          (A) ADDRESSEE: RATNER & PRESTIA

15   (B) STREET: P.O. BOX 980

          (C) CITY: VALLEY FORGE

          (D) STATE: PA

          (E) COUNTRY: USA

          (F) ZIP: 19482

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      (v) COMPUTER READABLE FORM:

          (A) MEDIUM TYPE: Diskette

          (B) COMPUTER: IBM Compatible

          (C) OPERATING SYSTEM: DOS

25   (D) SOFTWARE: FastSEQ for Windows Version 2.0

      (vi) CURRENT APPLICATION DATA:

          (A) APPLICATION NUMBER: TO BE ASSIGNED

          (B) FILING DATE: 09-MAY-1997

30   (C) CLASSIFICATION: Unknown

      (vii) PRIOR APPLICATION DATA:

          (A) APPLICATION NUMBER: 60/041,230

          (B) FILING DATE: 14-MAR-1997

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         (viii) ATTORNEY/AGENT INFORMATION:

            (A) NAME: PRESTIA, PAUL F.

            (B) REGISTRATION NUMBER: 23,031

5   (C) REFERENCE/DOCKET NUMBER: GH-50008

         (ix) TELECOMMUNICATION INFORMATION:

            (A) TELEPHONE: 610-407-0700

            (B) TELEFAX: 610-407-0701

10   (C) TELEX: 846169

         (2) INFORMATION FOR SEQ ID NO:1:

15   (i) SEQUENCE CHARACTERISTICS:

            (A) LENGTH: 3,881 base pairs

            (B) TYPE: nucleic acid

            (C) STRANDEDNESS: single

            (D) TOPOLOGY: linear

20   (ii) MOLECULE TYPE: cDNA

         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:


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CTTTGCGCCC ACAAAATACA CCGACGATGC CCGATCTACT TTAAGGGCTG AAACCCACGG      60
GCCTGAGAGA CTATAAGAGC GTTCCCTACC GCCATGGAAC AACGGGGACA GAACGCCCCG     120
GCCGCTTCGG GGGCCCGGAA AAGGCACGGC CCAGGACCCA GGGAGGCGCG GGGAGCCAGG     180
CCTGGGCCCC GGGTCCCCAA GACCCTTGTG CTCGTTGTCG CCGCGGTCCT GCTGTTGGTC     240
TCAGCTGAGT CTGCTCTGAT CACCCAACAA GACCTAGCTC CCCAGCAGAG AGCGGCCCCA     300
CAACAAAAGA GGTCCAGCCC CTCAGAGGGA TTGTGTCCAC CTGGACACCA TATCTCAGAA     360
GACGGTAGAG ATTGCATCTC CTGCAAATAT GGACAGGACT ATAGCACTCA ATGGAATGAC     420
CTCCTTTTCT GCTTGCGCTG CACCAGGTGT GATTCAGGTG AAGTGGAGCT AAGTCCCTGC     480
ACCACGACCA GAAACACAGT GTGTCAGTGC GAAGAAGGCA CCTTCCGGGA AGAAGATTCT     540
CCTGAGATGT GCCGGAAGTG CCGCACAGGG TGTCCCAGAG GGATGGTCAA GGTCGGTGAT     600
TGTACACCCT GGAGTGACAT CGAATGTGTC CACAAAGAAT CAGGCATCAT CATAGGAGTC     660
ACAGTTGCAG CCGTAGTCTT GATTGTGGCT GTGTTTGTTT GCAAGTCTTT ACTGTGGAAG     720
AAAGTCCTTC CTTACCTGAA AGGCATCTGC TCAGGTGGTG GTGGGGACCC TGAGCGTGTG     780
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GACAGAAGCT CACAACGACC TGGGGCTGAG GACAATGTCC TCAATGAGAT CGTGAGTATC    840

TTGCAGCCCA CCCAGGTCCC TGAGCAGGAA ATGGAAGTCC AGGAGCCAGC AGAGCCAACA    900

GGTGTCAACA TGTTGTCCCC CGGGGAGTCA GAGCATCTGC TGGAACCGGC AGAAGCTGAA    960

AGGTCTCAGA GGAGGAGGCT GCTGGTTCCA GCAAATGAAG GTGATCCCAC TGAGACTCTG   1020

AGACAGTGCT TCGATGACTT TGCAGACTTG GTGCCCTTTG ACTCCTGGGA GCCGCTCATG   1080

AGGAAGTTGG GCCTCATGGA CAATGAGATA AAGGTGGCTA AAGCTGAGGC AGCGGGCCAC   1140

AGGGACACCT TGTACACGAT GCTGATAAAG TGGGTCAACA AAACCGGGCG AGATGCCTCT   1200

GTCCACACCC TGCTGGATGC CTTGGAGACG CTGGGAGAGA GACTTGCCAA GCAGAAGATT   1260

GAGGACCACT TGTTGAGCTC TGGAAAGTTC ATGTATCTAG AAGGTAATGC AGACTCTGCC   1320

ATGTCCTAAG TGTGATTCTC TTCAGGAAGT CAGACCTTCC CTGGTTTACC TTTTTTCTGG   1380

AAAAAGCCCA ACTGGACTCC AGTCAGTAGG AAAGTGCCAC AATTGTCACA TGACCGGTAC   1440

TGGAAGAAAC TCTCCCATCC AACATCACCC AGTGGATGGA ACATCCTGTA ACTTTTCACT   1500

GCACTTGGCA TTATTTTTAT AAGCTGAATG TGATAATAAG GACACTATGG AAATGTCTGG   1560

ATCATTCCGT TTGTGCGTAC TTTGAGATTT GGTTTGGGAT GTCATTGTTT TCACAGCACT   1620

TTTTTATCCT AATGTAAATG CTTTATTTAT TTATTTGGGC TACATTGTAA GATCCATCTA   1680

CACAGTCGTT GTCCGACTTC ACTTGATACT ATATGATATG AACCTTTTTT GGGTGGGGGG   1740

TGCGGGGCAG TTCACTCTGT CTCCCAGGCT GGAGTGCAAT GGTGCAATCT TGGCTCACTA   1800

TAGCCTTGAC CTCTCAGGCT CAAGCGATTC TCCCACCTCA GCCATCCAAA TAGCTGGGAC   1860

CACAGGTGTG CACCACCACG CCCGGCTAAT TTTTTGTATT TTGTCTAGAT ATAGGGGCTC   1920

TCTATGTTGC TCAGGGTGGT CTCGAATTCC TGGACTCAAG CAGTCTGCCC ACCTCAGACT   1980

CCCAAAGCGG TGGAATTAGA GGCGTGAGCC CCCATGCTTG GCCTTACCTT TCTACTTTTA   2040

TAATTCTGTA TGTTATTATT TTATGAACAT GAAGAAACTT TAGTAAATGT ACTTGTTTAC   2100

ATAGTTATGT GAATAGATTA GATAAACATA AAAGGAGGAG ACATACAATG GGGGAAGAAG   2160

AAGAAGTCCC CTGTAAGATG TCACTGTCTG GGTTCCAGCC CTCCCTCAGA TGTACTTTGG   2220

CTTCAATGAT TGGCAACTTC TACAGGGGCC AGTCTTTTGA ACTGGACAAC CTTACAAGTA   2280

TATGAGTATT ATTTATAGGT AGTTGTTTAC ATATGAGTCG GGACCAAAGA GAACTGGATC   2340

CACGTGAAGT CCTGTGTGTG GCTGGTCCCT ACCTGGGCAG TCTCATTTGC ACCCATAGCC   2400

CCCATCTATG GACAGGCTGG GACAGAGGCA GATGGGTTAG ATCACACATA ACAATAGGGT   2460

CTATGTCATA TCCCAAGTGA ACTTGAGCCC TGTTTGGGCT CAGGAGATAG AAGACAAAAT   2520

CTGTCTCCCC ACGTCTGCCA TGGCATCAAG GGGGAAGAGT AGATGGTGCT TGAGAATGGT   2580

GTGAAATGGT TGCCATCTCA GGAGTAGATG GCCCGGCTCA CTTCTGGTTA TCTGTCACCC   2640

TGAGCCCATG AGCTGCCTTT TAGGGTACAG ATTGCCTACT TGAGGACCTT GGCCGCTCTG   2700

TAAGCATCTG ACTCATCTCA GAAATGTCAA TTCTTAAACA CTGTGGCAAC AGGACCTAGA   2760

ATGGCTGACG CATTAAGGTT TTCTTCTTGT GTCCTGTTCT ATTATTGTTT TAAGACCTCA   2820

GTAACCATTT CAGCCTCTTT CCAGCAAACC CTTCTCCATA GTATTTCAGT CATGGAAGGA   2880

TCATTTATGC AGGTAGTCAT TCCAGGAGTT TTTGGTCTTT TCTGTCTCAA GGCATTGTGT   2940
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GTTTTGTTCC GGGACTGGTT TGGGTGGGAC AAAGTTAGAA TTGCCTGAAG ATCACACATT    3000
CAGACTGTTG TGTCTGTGGA GTTTTAGGAG TGGGGGGTGA CCTTTCTGGT CTTTGCACTT    3060
CCATCCTCTC CCACTTCCAT CTGGCATCCC CACGCGTTGT CCCCTGCACT TCTGGAAGGC    3120
ACAGGGTGCT GCTGCTTCCT GGTCTTTGCC TTTGCTGGGC CTTCTGTGCA GGACGCTCAG    3180
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CCTCAGGGCT CAGAAGGTGC CAGTCCGGTC CCAGGTCCCT TGTCCCTTCC ACAGAGGCCT    3240
TCCTAGAAGA TGCATCTAGA GTGTCAGCCT TATCAGTGTT TAAGATTTTT CTTTTATTTT    3300
TAATTTTTTT GAGACAGAAT CTCACTCTCT CGCCCAGGCT GGAGTGCAAC GGTACGATCT    3360
TGGCTCAGTG CAACCTCCGC CTCCTGGGTT CAAGCGATTC TCGTGCCTCA GCCTCCGGAG    3420
TAGCTGGGAT TGCAGGCACC CGCCACCACG CCTGGCTAAT TTTTGTATTT TTAGTAGAGA    3480
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10
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CGGGGTTTCA CCATGTTGGT CAGGCTGGTC TCGAACTCCT GACCTCAGGT GATCCACNTT    3540
GGCCTCCGAA AGTGCTGGGA TATACAAGGC GTGAGCCACC AGCCAGGCCA AGATATTNTT    3600
NTAAAGNNAG CTTCCGGANG ACATGAAATA ANGGGGGGTT TTGTTGTTTA GTAACATTNG    3660
GCTTTGATAT ATCCCCAGGC CAAATNGCAN GNGACACAGG ACAGCCATAG TATAGTGTGT    3720
CACTCGTGGT TGGTGTCCTT TCATGGTTCT GCCCTGTCAA AGGTCCCTAT TTGAAATGTG    3780
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15
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TTATAATACA AACAAGGAAG CACATTGTGT ACAAAATACT TATGTATTTA TGAATCCATG    3840
ACCAAATTAA ATATGAAACC TTATATAAAA AAAAAAAAAA A                       3881
```

    (2) INFORMATION FOR SEQ ID NO:2:

20

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 411 amino acids
            (B) TYPE: amino acid
            (C) STRANDEDNESS: single
25   (D) TOPOLOGY: linear
        (ii) MOLECULE TYPE: protein

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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            Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg Lys
            1   5   10   15
            Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro Gly Pro
                            20   25   30
35   Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val Leu Leu Leu
                            35   40   45
            Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln
                            50   55   60

```
Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu
 65              70              75              80
Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp Cys Ile Ser
             85              90              95
Cys Lys Tyr Gly Gln Asp Tyr Ser Thr Gln Trp Asn Asp Leu Leu Phe
            100             105             110
Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val Glu Leu Ser Pro
            115             120             125
Cys Thr Thr Thr Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe
    130             135             140
Arg Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr Gly Cys
145             150             155             160
Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile
            165             170             175
Glu Cys Val His Lys Glu Ser Gly Ile Ile Ile Gly Val Thr Val Ala
            180             185             190
Ala Val Val Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp
            195             200             205
Lys Lys Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly Gly
    210             215             220
Asp Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp
225             230             235             240
Asn Val Leu Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val Pro
            245             250             255
Glu Gln Glu Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly Val Asn
            260             265             270
Met Leu Ser Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala Glu Ala
    275             280             285
Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala Asn Glu Gly Asp
    290             295             300
Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val
305             310             315             320
Pro Phe Asp Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp
            325             330             335
Asn Glu Ile Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr
            340             345             350
Leu Tyr Thr Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg Asp Ala
            355             360             365
Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr Leu Gly Glu Arg Leu
    370             375             380
Ala Lys Gln Lys Ile Glu Asp His Leu Leu Ser Ser Gly Lys Phe Met
385             390             395             400
```

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```
      Tyr Leu Glu Gly Asn Ala Asp Ser Ala Met Ser End
                    405                 410 411
```

5   (2) INFORMATION FOR SEQ ID NO:3:

        (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 1062 base pairs

        (B) TYPE: nucleic acid

10   (C) STRANDEDNESS: single

        (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: cDNA

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

15

```
ATGACCTCCT TTTCTGCTTG CGCTGCACCA GGTGTGATTC AGGTGAAGTG GAGCTAAGTC     60
CCTGCACCAC GACCAGAAAC ACAGTGTGTC AGTGCGAAGA AGGCACCTTC CGGGAAGAAG    120
ATTCTCCTGA GATGTGCCGG AAGTGCCGCA CAGGGTGTCC CAGAGGGATG GTCAAGGTCG    180
GTGATTGTAC ACCCTGGAGT GACATCGAAT GTGTCCACAA AGAATCAGGC ATCATCATAG    240
GAGTCACAGT TGCAGCCGTA GTCTTGATTG TGGCTGTGTT TGTTTGCAAG TCTTTACTGT    300
GGAAGAAAGT CCTTCCTTAC CTGAAAGGCA TCTGCTCAGG TGGTGGTGGG GACCCTGAGC    360
GTGTGGACAG AAGCTCACAA CGACCTGGGG CTGAGGACAA TGTCCTCAAT GAGATCGTGA    420
GTATCTTGCA GCCCACCCAG GTCCCTGAGC AGGAAATGGA AGTCCAGGAG CCAGCAGAGC    480
CAACAGGTGT CAACATGTTG TCCCCCGGGG AGTCAGAGCA TCTGCTGGAA CCGGCAGAAG    540
CTGAAAGGTC TCAGAGGAGG AGGCTGCTGG TTCCAGCAAA TGAAGGTGAT CCCACTGAGA    600
CTCTGAGACA GTGCTTCGAT GACTTTGCAG ACTTGGTGCC CTTTGACTCC TGGGAGCCGC    660
TCATGAGGAA GTTGGGCCTC ATGGACAATG AGATAAAGGT GGCTAAAGCT GAGGCAGCGG    720
GCCACAGGGA CACCTTGTAC ACGATGCTGA TAAAGTGGGT CAACAAAACC GGGCGAGATG    780
CCTCTGTCCA CACCCTGCTG GATGCCTTGG AGACGCTGGG AGAGAGACTT GCCAAGCAGA    840
AGATTGAGGA CCACTTGTTG AGCTCTGGAA AGTTCATGTA TCTAGAAGGT AATGCAGACT    900
CTGCCATGTC CTAAGTGTGA TTCTCTTCAG GAAGTCAGAC CTTCCCTGGT TTACCTTTTT    960
TCTGGAAAAA GCCCAACTGG ACTCCAGTCA GTAGGAAAGT GCCACAATTG TCACATGACC   1020
GGTACTGGAA GAAACTCTCC CATCCAACAT CACCCAGTGG AT                      1062
```

35   (2) INFORMATION FOR SEQ ID NO:4:

        (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 303 amino acids

        (B) TYPE: amino acid

40   (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
Asp Leu Leu Phe Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val
1               5                   10                  15
Glu Leu Ser Pro Cys Thr Thr Thr Arg Asn Thr Val Cys Gln Cys Glu
                20                  25                  30
Glu Gly Thr Phe Arg Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys
            35                  40                  45
Arg Thr Gly Cys Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro
        50                  55                  60
Trp Ser Asp Ile Glu Cys Val His Lys Glu Ser Gly Ile Ile Ile Gly
65                  70                  75                  80
Val Thr Val Ala Ala Val Val Leu Ile Val Ala Val Phe Val Cys Lys
                85                  90                  95
Ser Leu Leu Trp Lys Lys Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser
                100                 105                 110
Gly Gly Gly Gly Asp Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro
            115                 120                 125
Gly Ala Glu Asp Asn Val Leu Asn Glu Ile Val Ser Ile Leu Gln Pro
        130                 135                 140
Thr Gln Val Pro Glu Gln Glu Met Glu Val Gln Glu Pro Ala Glu Pro
145                 150                 155                 160
Thr Gly Val Asn Met Leu Ser Pro Gly Glu Ser Glu His Leu Leu Glu
                165                 170                 175
Pro Ala Glu Ala Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala
            180                 185                 190
Asn Glu Gly Asp Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp Asp Phe
            195                 200                 205
Ala Asp Leu Val Pro Phe Asp Ser Trp Glu Pro Leu Met Arg Lys Leu
        210                 215                 220
Gly Leu Met Asp Asn Glu Ile Lys Val Ala Lys Ala Glu Ala Ala Gly
225                 230                 235                 240
His Arg Asp Thr Leu Tyr Thr Met Leu Ile Lys Trp Val Asn Lys Thr
                245                 250                 255
Gly Arg Asp Ala Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr Leu
            260                 265                 270
Gly Glu Arg Leu Ala Lys Gln Lys Ile Glu Asp His Leu Leu Ser Ser
            275                 280                 285
```

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Gly Lys Phe Met Tyr Leu Glu Gly Asn Ala Asp Ser Ala Met Ser
        290   295   300